

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=5; day=3; hr=16; min=14; sec=47; ms=293;]

=====

Application No: 10535522 Version No: 4.0

Input Set:

Output Set:

Started: 2010-04-27 12:46:08.469
Finished: 2010-04-27 12:46:09.867
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 398 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 14
Actual SeqID Count: 14

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for
the Treatment or Prevention of Diseases

<130> 032723woJH

<140> 10535522

<141> 2006-04-13

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(615)

<400> 1

atg	tcg	cg	g	g	ctc	cag	ctt	ctg	ctc	ctg	agc	tgc	gcc	tac	agc	ctg	48
Met	Ser	Arg	Gly	Leu	Gln	Leu	Leu	Leu	Leu	Ser	Cys	Ala	Tyr	Ser	Leu		
1				5						10					15		

gct	ccc	gcg	acg	ccg	gag	gtg	aag	gtg	gct	tgc	tcc	gaa	gat	gtg	gac	96
Ala	Pro	Ala	Thr	Pro	Glu	Val	Lys	Val	Ala	Cys	Ser	Glu	Asp	Val	Asp	
			20					25						30		

ttg	ccc	tgc	acc	gcc	ccc	tgg	gat	ccg	cag	gtt	ccc	tac	acg	gtc	tcc	144
Leu	Pro	Cys	Thr	Ala	Pro	Trp	Asp	Pro	Gln	Val	Pro	Tyr	Thr	Val	Ser	
		35					40					45				

tgg	gtc	aag	tta	ttg	gag	ggt	ggt	gaa	gag	agg	atg	gag	aca	ccc	cag	192
Trp	Val	Lys	Leu	Leu	Glu	Gly	Gly	Glu	Glu	Arg	Met	Glu	Thr	Pro	Gln	
	50					55				60						

gaa	gac	cac	ctc	agg	gga	cag	cac	tat	cat	cag	aag	ggg	caa	aat	ggt	240
Glu	Asp	His	Leu	Arg	Gly	Gln	His	Tyr	His	Gln	Lys	Gly	Gln	Asn	Gly	
65					70					75					80	

tct	ttc	gac	gcc	ccc	aat	gaa	agg	ccc	tat	tcc	ctg	aag	atc	cga	aac	288
Ser	Phe	Asp	Ala	Pro	Asn	Glu	Arg	Pro	Tyr	Ser	Leu	Lys	Ile	Arg	Asn	
				85					90						95	

act	acc	agc	tgc	aac	tcg	ggg	aca	tac	agg	tgc	act	ctg	cag	gac	ccg	336
Thr	Thr	Ser	Cys	Asn	Ser	Gly	Thr	Tyr	Arg	Cys	Thr	Leu	Gln	Asp	Pro	
			100					105					110			

gat	ggg	cag	aga	aac	cta	agt	ggc	aag	gtg	atc	ttg	aga	gtg	aca	gga	384
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly	
115 120 125	
tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag	432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu	
130 135 140	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att	480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile	
145 150 155 160	
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct	528
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser	
165 170 175	
aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag	576
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys	
180 185 190	
cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga	618
His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val	
195 200 205	
<210> 2	
<211> 205	
<212> PRT	
<213> Homo sapiens	
<400> 2	
Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu	
1 5 10 15	
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp	
20 25 30	
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser	
35 40 45	
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln	
50 55 60	
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly	
65 70 75 80	
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn	
85 90 95	
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro	
100 105 110	

Asp	Gly	Gln	Arg	Asn	Leu	Ser	Gly	Lys	Val	Ile	Leu	Arg	Val	Thr	Gly
	115						120					125			

Cys	Pro	Ala	Gln	Arg	Lys	Glu	Glu	Thr	Phe	Lys	Lys	Tyr	Arg	Ala	Glu
	130					135					140				

Ile	Val	Leu	Leu	Leu	Ala	Leu	Val	Ile	Phe	Tyr	Leu	Thr	Leu	Ile	Ile
145					150				155					160	

Phe	Thr	Cys	Lys	Phe	Ala	Arg	Leu	Gln	Ser	Ile	Phe	Pro	Asp	Phe	Ser
			165						170					175	

Lys	Ala	Gly	Met	Glu	Arg	Ala	Phe	Leu	Pro	Val	Thr	Ser	Pro	Asn	Lys
		180						185					190		

His	Leu	Gly	Leu	Val	Thr	Pro	His	Lys	Thr	Glu	Leu	Val
	195						200				205	

<210> 3
 <211> 2051
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (14)..(601)

<400> 3	
gcgctccagc cgc atg tcg caa ggc ctc cag ctc ctg ttt cta ggc tgc	49
Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys	
1 5 10	
gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct	97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala	
15 20 25	
tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag	145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln	
30 35 40	
ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag	193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu	
45 50 55 60	
agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc	241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro	
65 70 75	

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc	289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser	
80 85 90	
tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac	337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn	
95 100 105	
ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct	385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala	
110 115 120	
aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc	433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe	
125 130 135 140	
tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt	481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe	
145 150 155	
gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa	529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu	
160 165 170	
caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg	577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val	
175 180 185	
acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttaciaaag	631
Thr Leu Pro Lys Thr Glu Thr Val	
190 195	
ccaagggcac atcagatcag tgtgcttgaa tgccacccgg acaagagaag aatgagctcc	691
atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc	751
cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct	811
ctgtggctgt cagcttaatg tttcatgtgg ctatctggtc aacctcgtga gtgcttttca	871
gtcatctaca agctatggtg agatgcaggt gaagcagggg catgggaaat ttgaacactc	931
tgagctggcc ctgtgacaga ctctgagga cagctgtcct ctctacatc tgggatacat	991
ctctttgaat ttgtcctgtt tcgttgacc agccagatg tctcacatct ggcgaaatt	1051
gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt	1111
cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc	1171
cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca	1231
catttatattt tttaatcttc atgtacttgt caaagaagaa ttttcatgt tttttcaaag	1291
aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga	1351
caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca	1411

ctgtacagtg cctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471
 aagattgtct gtatgattct ggacgagtca cttgtggttt tcactctctg gttagtaaac 1531
 cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg 1591
 tagtgaatac attggcaact ctactgggct gttaccttgt tgatatacta gagttctgga 1651
 gctgagcgaa tgectgtcat atctcagctt gcccatcaat ccaaacacag gaggctacaa 1711
 aaaggacatg agcatgggtct tctgtgtgaa ctctctctga gaaacgtgga gactggctca 1771
 gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat 1831
 tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt 1891
 taatgagctg ggctccttcc tcatttgctt ccaaagaga ttttgcacca ctaatggtgt 1951
 gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011
 tcagccatga ctttcatgct attaaaagaa tgcattgtgaa 2051

<210> 4
 <211> 196
 <212> PRT
 <213> Mus musculus

<400> 4

Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys Ala Cys Ser Leu
 1 5 10 15

Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala Cys Ser Glu Thr
 20 25 30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
 35 40 45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
 50 55 60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
 65 70 75 80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
 85 90 95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
 100 105 110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
115 120 125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145 150 155 160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
165 170 175

Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
180 185 190

Thr Glu Thr Val
195

<210> 5
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer for CD83ext

<400> 5
tcccccgagg acgccggagg tgaaggtggc t 31

<210> 6
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer for CD83ext

<400> 6
aattagaatt ctcaaattctc cgctctgtat t 31

<210> 7
<211> 435
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic partial sequence of pGEX2ThCD83ext


```

<220>
<221> CDS
<222> (1)..(417)

<220>
<221> mat_peptide
<222> (28)..(417)

<400> 7
cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag      48
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
          -5          -1  1          5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc      96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
          10          15          20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag      144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
          25          30          35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga      192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40          45          50          55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat      240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
          60          65          70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg      288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
          75          80          85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta      336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
          90          95          100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa      384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
          105          110          115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact      435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120          125          130

<210> 8
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 8

```

Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
 -5 -1 1 5

Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
 10 15 20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
 25 30 35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
 60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
 75 80 85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
 105 110 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 9
 <211> 435
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic partial sequence of pGEX2ThCD83ext_mut129_CtoS

<220>
 <221> CDS
 <222> (1)..(417)

<220>
 <221> mat_peptide
 <222> (28)..(417)

<400> 9
 cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag
 Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu

-5	-1	1	5	
gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc				96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro				
10	15		20	
tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag				144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu				
25	30		35	
ggg ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga				192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly				
40	45		50	55
cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat				240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn				
60	65		70	
gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg				288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser				
75	80		85	
ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta				336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu				
90				